

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:39 ; Search time 2351.15 Seconds

(without alignments)
154.366 Million cell updates/sec

Title: US-09-851-670-13

Perfect score: 22

Sequence: 1 caccgcctctcgcacatgga 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 segs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_da:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_vi:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13.4	60.9	41	6	A93667	A93667 Sequence 3
2	13	59.1	37	6	A98891	A98891 Sequence 9
3	12.8	58.2	35	6	AR059842	AR059842 Sequence
4	12.8	58.2	57	9	S57433	S57433 T-cell-rece
5	12.6	57.3	37	6	A98888	A98888 Sequence 6
6	12.6	57.3	48	3	HC084486	HC084486 Haemochus
7	12.6	57.3	58	6	118948	118948 Sequence 30
8	12.6	57.3	58	6	118949	118949 Sequence 31
9	12.6	57.3	58	6	124133	124133 Sequence 30
10	12.6	57.3	58	6	124134	124134 Sequence 31
11	12.4	56.4	40	6	AR150948	AR150948 Sequence
12	12.4	56.4	42	6	AR123052	AR123052 Sequence
13	12.4	56.4	51	6	AR118585	AR118585 Sequence
14	12.2	55.5	27	6	AR153624	AR153624 Sequence
15	12.2	55.5	51	6	A42067	A42067 Sequence 10
16	12.2	55.5	51	6	AX160849	AX160849 Sequence
17	12.2	55.5	60	6	AR0463	AR0463 Sequence 23
18	12	54.5	31	6	140626	140626 Sequence 3
19	12	54.5	49	6	108645	108645 Sequence 1
20	12	54.5	51	9	S78430	S78430 Homo sapien
21	12	54.5	57	9	HSTCK6X13	HSTCK6X13 Sequence
22	12	54.5	57	9	HSTCK6X35	HSTCK6X35 Sequence
23	12	54.5	57	9	HSTCK6X36	HSTCK6X36 Sequence
24	12	54.5	57	9	HSTCK6X13	HSTCK6X13 Sequence
25	12	54.5	57	9	HSTCK6X35	HSTCK6X35 Sequence
26	12	54.5	57	9	HSTCK6X36	HSTCK6X36 Sequence
27	11.8	53.6	26	6	179834	179834 Sequence 19
28	11.8	53.6	32	6	AR054995	AR054995 Sequence
29	11.8	53.6	32	6	AR156244	AR156244 Sequence
30	11.8	53.6	36	6	186428	186428 Sequence 36
31	11.6	52.7	20	6	AR129487	AR129487 Sequence
32	11.6	52.7	20	6	E31432	E31432 Gene partic
33	11.6	52.7	27	6	AR008922	AR008922 Sequence
34	11.6	52.7	27	6	AR087617	AR087617 Sequence
35	11.6	52.7	28	6	182037	182037 Sequence 75
36	11.6	52.7	28	6	191725	191725 Sequence 75
37	11.6	52.7	35	6	AI7073	AI7073 Oligonucleo
38	11.6	52.7	35	6	AI7074	AI7074 Oligonucleo
39	11.6	52.7	35	6	AI7471	AI7471 Oligonucleo
40	11.6	52.7	35	6	AI7472	AI7472 Oligonucleo
41	11.6	52.7	35	6	A23883	A23883 Oligonucleo
42	11.6	52.7	35	6	A23899	A23899 Oligonucleo
43	11.6	52.7	35	6	AR014441	AR014441 Sequence
44	11.6	52.7	35	6	AR014450	AR014450 Sequence
45	11.6	52.7	35	6	AR059828	AR059828 Sequence

ALIGNMENTS

RESULT 1

A93667/c

LOCUS A93667 41 bp DNA

DEFINITION Sequence 3 from Patent WO9734144.

ACCESSION A93667

VERSION A93667.1 GI:6741855

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

artificial sequence.

REFERENCE

1 (bases 1 to 41)

LANGER, G. and TOSCHL, L.

TITLE

METHOD OF DETECTING THE EFFECT OF TEST SUBSTANCES USING HEN UROKINASE

JOURNAL

Patent: WO 9734144-A 3 18-SEP-1997;

SCHERING AG (DE); LANGER GERNOT (DE)

AUTHORS

Location/Qualifiers

FEATURES

source

1..41

/organism="synthetic construct"

/db_xref="taxon:32630"

22-JAN-2000

BASE COUNT 5 a 14 c 15 g 7 t
ORIGIN

Query Match 60.9%; Score 13.4; DB 6; Length 41;
Best Local Similarity 93.3%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 caccgcgtctctcga 15
Db 31 CACCCGCTTCGCA 17

RESULT 2

LOCUS A98891 37 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 9 from Patent WO909211.
ACCESSION A98891
VERSION A98891.1 GI:6781850
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Coutts,J.C. and Oultram,J.D.
TITLE AMPLIFICATION OF NUCLEIC ACIDS
JOURNAL Patent: WO 909211-A 9 25-FEB-1999;
COUTTS JACQUELINE CLARE (GB); OULTRAM JOHN DOUGLAS (GB)

FEATURES
source 1..37
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 9 a 8 c 9 g 11 t
ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 37;
Best Local Similarity 76.2%; Pred. No. 2.7e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 accgcgtctctcgacaatga 22
Db 8 AACCACTGCTCGACGCTGA 28

RESULT 3
LOCUS AR059842 35 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 50 from patent US 5840521.
ACCESSION AR059842
VERSION AR059842.1 GI:5986292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Barth,P.Thomas.
TITLE Expression vector containing an inducible selection gene system
JOURNAL Patent: US 5840521-A 50 24-NOV-1998;
FEATURES
source 1..35
/organism="unknown"

BASE COUNT 10 a 7 c 9 g 9 t
ORIGIN

Query Match 58.2%; Score 12.8; DB 6; Length 35;
Best Local Similarity 87.5%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 gctctcgcacaatgg 21
Db 22 GCTCTCTAGACCATGG 7

RESULT 4

LOCUS S57433 57 bp mRNA PRI 07-MAY-1993
DEFINITION T-cell-receptor Valpha 17.2 segment [human, mRNA Partial, 57 nt].
ACCESSION S57433
VERSION S57433.1 GI:236318
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 57)
AUTHORS Nematsu,Y., Wege,H., Straus,A., Ott,M., Bannwarch,W., Lanchbury,J.,
Panayl.G. and Steinmetz,M.
TITLE The T-cell-receptor repertoire in the synovial fluid of a patient
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8534-8538 (1991)
MEDLINE 9202087
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI glibsg 57433] from the original journal article.
This sequence comes from Fig 3.

FEATURES

source 1..57
/organism="Homo sapiens"
/db_xref="taxon:9606"
1..57
/partial
/gene="T-cell-receptor Valpha 17.2 segment"
1..57
/partial
/gene="T-cell-receptor Valpha 17.2 segment"
1..57
/note="This sequence comes from Fig 3"

CDS

1..57
/product="T-cell-receptor variable region alpha chain C
terminus"
/protein_id="AAB19956.1"
/db_xref="GI:236319"
/translation="LSLDIVPSQPDSDANYFCA"
BASE COUNT 8 a 20 c 12 g 17 t
ORIGIN

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Best Local Similarity 87.5%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 cgctctcgcacaatg 20
Db 1 CTCTCTCGACATGG 16

RESULT 5
LOCUS A98888 37 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 6 from Patent WO909211.
ACCESSION A98888
VERSION A98888.1 GI:6781847
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Coutts,J.C. and Oultram,J.D.
TITLE AMPLIFICATION OF NUCLEIC ACIDS
JOURNAL Patent: WO 909211-A 6 25-FEB-1999;
COUTTS JACQUELINE CLARE (GB); OULTRAM JOHN DOUGLAS (GB)

FEATURES

source 1..37
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 10 c 10 g 11 t

ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 ccgcctctcgacacatg 22
||| ||||| |||
Db 10 CCACTCTCTGACGTGGA 28

RESULT 6

LOCUS HCU84486 48 bp DNA INV 22-SEP-1997
DEFINITION Haemonchus contortus CT microsatellite DNA sequence.
ACCESSION U84486
VERSION U84486.1 GI:2429139
KEYWORDS
SOURCE Haemonchus contortus.
ORGANISM Haemonchus contortus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.

REFERENCE 1 (bases 20 to 29)
Hoekstra, R., Criado-Fornelio, A., Fakeldi, J., Bergman, J. and
Roos, M. H.

TITLE Microsatellites of the parasitic nematode Haemonchus contortus:
polymorphism and linkage with a direct repeat
Mol. Biochem. Parasitol. 89 (1), 97-107 (1997)
97442739

REFERENCE 2 (bases 1 to 48)
Hoekstra, R.
Direct Submission
Submitted (09-JAN-1997) Institute for Animal Science and Health
(ID-DIO), Molecular Recognition, Edelhertweg 15, Lelystad 8200 Ab,
The Netherlands

FEATURES
Location/Qualifiers
source 1..48

repeat_region
/organism="Haemonchus contortus"
/db_xref="taxon:6289"
20..29
/note="microsatellite; imperfect"
/rpt_type=tandem
/rpt_unit=CT
/evidence=experimental

BASE COUNT 14 a 15 c 6 g 13 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 3; Length 48;
Best Local Similarity 78.9%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 accgcctctcgacacatg 20
||| ||||| |||
Db 19 ACTCTCTCTCAATATG 37

RESULT 7

LOCUS I18948 58 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 30 from patent US 5501962.
ACCESSION I18948
VERSION I18948.1 GI:1599303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 58)
Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and
Ollins, P.O.
Interleukin-3 (IL-3) human/murine hybrid polypeptides and
recombinant production of the same

JOURNAL Patent: US 5501962-A 30 26-MAR-1996;
FEATURES Location/Qualifiers
source 1..58

BASE COUNT 13 a 20 c 15 g 10 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;
Best Local Similarity 78.9%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 caccgcctctcgacacat 19
||| ||||| |||
Db 14 CATCCGCTCTGCCCAAT 32

RESULT 8

LOCUS I18949/C 58 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 31 from patent US 5501962.
ACCESSION I18949
VERSION I18949.1 GI:1599304
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 58)
Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and
Ollins, P.O.
Interleukin-3 (IL-3) human/murine hybrid polypeptides and
recombinant production of the same
Patent: US 5501962-A 31 26-MAR-1996;
Location/Qualifiers
source 1..58

FEATURES
Location/Qualifiers
BASE COUNT 11 a 14 c 19 g 14 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;
Best Local Similarity 78.9%; Pred. No. 4.5e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 caccgcctctcgacacat 19
||| ||||| |||
Db 49 CATCCGCTCTGCCCAAT 31

RESULT 9
LOCUS I24133 58 bp DNA PAT 07-OCT-1996
DEFINITION Sequence 30 from patent US 5543141.
ACCESSION I24133
VERSION I24133.1 GI:1604003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 58)
Bratford-Goldberg, S.R., Easton, A.M., Klein, B.K., McKearn, J.P. and
Ollins, P.O.
Therapeutic methods using Interleukin-3 (IL-3) human/murine hybrid
polypeptides
Patent: US 5543141-A 30 06-AUG-1996;
Location/Qualifiers
source 1..58

FEATURES
Location/Qualifiers
BASE COUNT 13 a 20 c 15 g 10 t
ORIGIN

Query Match 57.3%; Score 12.6; DB 6; Length 58;

AUTHORS NISHI, K., HIKICHI, I. and SUMICAWA, I.

TITLE Fas ligand-like protein, its production and use
 JOURNAL Patent: US 6235878-A 24 22-MAY-2001;
 FEATURES Location/Qualifiers
 source 1..27
 BASE COUNT 8 a 9 c 3 g 7 t
 ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 27;
 Best Local Similarity 82.4%; Pred. No. 7.5e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 gctctctgcacatgga 22
 ||| | ||||| |||
 Db 26 GCTATGACGACATGGA 10

RESULT 15
 A42067/c A42067 51 bp DNA PAT 05-MAR-1997
 DEFINITION Sequence 10 from Patent WO9500637.
 A42067
 VERSION A42067.1 GI:2297559
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 51)
 AUTHORS Hansson,L.

JOURNAL TRANSGENIC PRODUCTION OF FC-SOD
 PATENT: WO 9500637-A 10 05-JAN-1995;
 SYMBICOM AB (SE)

COMMENT Other publication CA 2164089 950105
 Other publication AU 6935694 950117.

FEATURES Location/Qualifiers
 source 1..51

CDS
 1..24
 /db_xref="taxon:32644"
 /note="Protein sequence is in conflict with the conceptual
 translation"

/codon_start=1
 /product="C-TERMINAL OF VARIANT T213"
 /protein_id="CAA02648.1"
 /db_xref="GI:2297560"
 /translation="HSEKKK"
 BASE COUNT 14 a 14 c 19 g 4 t
 ORIGIN

Query Match 55.5%; Score 12.2; DB 6; Length 51;
 Best Local Similarity 82.4%; Pred. No. 7.5e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 caccgcgtctctgcaca 17
 ||| ||||| |||
 Db 38 CACTCGCTCTCGCGTCA 22

Search completed: March 9, 2002, 00:48:40
 Job time: 11121 sec

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